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Sequence Listing was accepted with existing errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: markspencer

Timestamp: Wed May 02 11:37:17 EDT 2007

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Application No: 10624945 Version No: 2.0

**Input Set:**

**Output Set:**

**Started:** 2007-04-24 07:01:13.338  
**Finished:** 2007-04-24 07:01:15.041  
**Elapsed:** 0 hr(s) 0 min(s) 1 sec(s) 703 ms  
**Total Warnings:** 3  
**Total Errors:** 8  
**No. of SeqIDs Defined:** 12  
**Actual SeqID Count:** 12

**ErrCode** **Error Description**

E 249	Order Sequence Error <140> -> <140>; Expected Mandatory Tag: <210> in Header
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
E 257	Invalid sequence data feature in <221> in SEQ ID (11)
E 257	Invalid sequence data feature in <221> in SEQ ID (11)
E 341	'Xaa' position not defined SEQID (11) POS (4)
E 341	'Xaa' position not defined SEQID (11) POS (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
E 257	Invalid sequence data feature in <221> in SEQ ID (12)
E 341	'Xaa' position not defined SEQID (12) POS (6)
E 250	Structural Validation Error; Sequence listing may not be indexable

SEQUENCE LISTING

<110> YEH, EDWARD T.H.  
GONG, LIMIN

<120> COMPOSITION AND METHODS RELATING TO SENP1-A  
SENTRIN-SPECIFIC PROTEASE

<130> UTSH:245USC1

<140> 10/624, 945  
<140> 2003-07-22

<150> 09/628, 966  
<151> 2000-07-31

<150> 60/146, 774  
<151> 1999-07-31

<160> 12

<170> PatentIn Ver. 2.1

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<212> DNA  
<213> Human

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<211> 643

<212> PRT

<213> Human

<400> 2

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Leu Val Asn His Asn Ser Val Phe Lys Thr His Leu Leu Pro Gln Thr  
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Gly Phe Pro Glu Asp Gln Leu Ser Leu Ser Asp Gln Gln Ile Leu Ser  
35 40 45

Ser Arg Gln Gly His Leu Asp Arg Ser Phe Thr Cys Ser Thr Arg Ser  
50 55 60

Ala Ala Tyr Asn Pro Ser Tyr Tyr Ser Asp Asn Pro Ser Ser Asp Ser  
65 70 75 80

Phe Leu Gly Ser Gly Asp Leu Arg Thr Phe Gly Gln Ser Ala Asn Gly  
85 90 95

Gln Trp Arg Asn Ser Thr Pro Ser Ser Ser Ser Leu Gln Lys Ser  
100 105 110

Arg Asn Ser Arg Ser Leu Tyr Leu Glu Thr Arg Lys Thr Ser Ser Gly  
115 120 125

Leu Ser Asn Ser Phe Ala Gly Lys Ser Asn His His Cys His Val Ser  
130 135 140

Ala Tyr Glu Lys Ser Phe Pro Ile Lys Pro Val Pro Ser Pro Ser Trp  
145 150 155 160

Ser Gly Ser Cys Arg Arg Ser Leu Leu Ser Pro Lys Lys Thr Gln Arg  
165 170 175

Arg His Val Ser Thr Ala Glu Glu Thr Val Gln Glu Glu Arg Glu  
180 185 190

Ile Tyr Arg Gln Leu Leu Gln Met Val Thr Gly Lys Gln Phe Thr Ile  
195 200 205

Ala Lys Pro Thr Thr His Phe Pro Leu His Leu Ser Arg Cys Leu Ser  
210 215 220

Ser Ser Lys Asn Thr Leu Lys Asp Ser Leu Phe Lys Asn Gly Asn Ser  
225 230 235 240

Cys Ala Ser Gln Ile Ile Gly Ser Asp Thr Ser Ser Ser Gly Ser Ala  
245 250 255

Ser Ile Leu Thr Asn Gln Glu Gln Leu Ser His Ser Val Tyr Ser Leu  
260 265 270

Ser Ser Tyr Thr Pro Asp Val Ala Phe Gly Ser Lys Asp Ser Gly Thr  
275 280 285

Leu His His Pro His His His Ser Val Pro His Gln Pro Asp Asn  
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Leu Lys Val Lys Asp Ser Gln Thr Pro Thr Pro Ser Ser Thr Phe Phe  
325 330 335

Gln Ala Glu Leu Trp Ile Lys Glu Leu Thr Ser Val Tyr Asp Ser Arg  
340 345 350

Ala Arg Glu Arg Leu Arg Gln Ile Glu Glu Gln Lys Ala Leu Ala Leu  
355 360 365

Gln Leu Gln Asn Gln Arg Leu Gln Glu Arg Glu His Ser Val His Asp  
370 375 380

Ser Val Glu Leu His Leu Arg Val Pro Leu Glu Lys Glu Ile Pro Val  
385 390 395 400

Thr Val Val Gln Glu Thr Gln Lys Lys Gly His Lys Leu Thr Asp Ser  
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Glu Asp Glu Phe Pro Glu Ile Thr Glu Glu Met Glu Lys Glu Ile Lys  
420 425 430

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435 440 445

Arg Leu Thr Ile Thr Arg Lys Asp Ile Gln Thr Leu Asn His Leu Asn  
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Trp Leu Asn Asp Glu Ile Ile Asn Phe Tyr Met Asn Met Leu Met Glu  
465 470 475 480

Arg Ser Lys Glu Lys Gly Leu Pro Ser Val His Ala Phe Asn Thr Phe  
485 490 495

Phe Phe Thr Lys Leu Lys Thr Ala Gly Tyr Gln Ala Val Lys Arg Trp  
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Thr Lys Lys Val Asp Val Phe Ser Val Asp Ile Leu Leu Val Pro Ile  
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His Leu Gly Val His Trp Cys Leu Ala Val Val Asp Phe Arg Lys Lys  
530 535 540

Asn Ile Thr Tyr Tyr Asp Ser Met Gly Gly Ile Asn Asn Glu Ala Cys  
545 550 555 560

Arg Ile Leu Leu Gln Tyr Leu Lys Gln Glu Ser Ile Asp Lys Lys Arg  
565 570 575

Lys Glu Phe Asp Thr Asn Gly Trp Gln Leu Phe Ser Lys Lys Ser Gln  
580 585 590

Ile Pro Gln Gln Met Asn Gly Ser Asp Cys Gly Met Phe Ala Cys Lys  
595 600 605

Tyr Ala Asp Cys Ile Thr Lys Asp Arg Pro Ile Asn Phe Thr Gln Gln  
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His Met Pro Tyr Phe Arg Lys Arg Met Val Trp Glu Ile Leu His Arg  
625 630 635 640

Lys Leu Leu

<210> 3  
<211> 9  
<212> PRT  
<213> Influenza virus

<400> 3  
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1 5

<210> 4  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
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<210> 5

<211> 28  
<212> DNA  
<213> Human

<400> 5  
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28

<210> 6  
<211> 25  
<212> DNA  
<213> Human

<400> 6  
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25

<210> 7  
<211> 2795  
<212> DNA  
<213> Human

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<211> 509

<212> PRT

<213> Human

<400> 8

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35 40 45

Asp Tyr Pro Lys Ile Arg Val Thr Val Thr Arg Asp Gln Pro Arg Arg  
50 55 60

Val Leu Pro Ser Phe Gly Phe Thr Leu Asn Ser Glu Gly Cys Asn Arg  
65 70 75 80

Arg Pro Gly Gly Arg Arg His Ser Lys Gly Asn Pro Glu Ser Ser Leu  
85 90 95

Met Trp Lys Pro Gln Glu Gln Ala Val Thr Glu Met Ile Ser Glu Glu  
100 105 110

Ser Gly Lys Gly Leu Arg Arg Pro His Cys Thr Val Glu Glu Gly Val  
115 120 125

Gln Lys Glu Glu Arg Glu Lys Tyr Arg Lys Leu Leu Glu Arg Leu Lys  
130 135 140

Glu Ser Gly His Gly Asn Ser Val Cys Pro Val Thr Ser Asn Tyr His  
145 150 155 160

Ser Ser Gln Arg Ser Gln Met Asp Thr Leu Lys Thr Lys Gly Trp Gly  
165 170 175

Glu Glu Gln Asn His Gly Val Lys Thr Thr Gln Phe Val Pro Lys Gln  
180 185 190

Tyr Arg Leu Val Glu Thr Arg Gly Pro Leu Cys Ser Leu Arg Ser Glu  
195 200 205

Lys Arg Cys Ser Lys Gly Lys Ile Thr Asp Thr Glu Lys Met Val Gly  
210 215 220

Ile Arg Phe Glu Asn Glu Ser Arg Arg Gly Tyr Gln Leu Glu Pro Asp  
225 230 235 240

Leu Ser Glu Glu Val Ser Ala Arg Leu Arg Leu Gly Ser Gly Ser Asn  
245 250 255

Gly Leu Leu Arg Arg Lys Val Ser Ile Ile Glu Thr Lys Glu Lys Asn  
260 265 270

Cys Ser Gly Lys Glu Arg Asp Arg Arg Thr Asp Asp Leu Leu Glu Leu  
275 280 285

Thr Glu Asp Met Glu Lys Glu Ile Ser Asn Ala Leu Gly His Gly Pro  
290 295 300

Gln Asp Glu Ile Leu Ser Ser Ala Phe Lys Leu Arg Ile Thr Arg Gly  
305 310 315 320

Asp Ile Gln Thr Leu Lys Asn Tyr His Trp Leu Asn Asp Glu Val Ile  
325 330 335

Asn Phe Tyr Met Asn Leu Leu Val Glu Arg Asn Lys Lys Gln Gly Tyr  
340 345 350

Pro Ala Leu His Val Phe Ser Thr Phe Phe Tyr Pro Lys Leu Lys Ser  
355 360 365

Gly Gly Tyr Gln Ala Val Lys Arg Trp Thr Lys Gly Val Asn Leu Phe  
370 375 380

Glu Gln Glu Ile Ile Leu Val Pro Ile His Arg Lys Val His Trp Ser  
385 390 395 400

Leu Val Val Ile Asp Leu Arg Lys Lys Cys Leu Lys Tyr Leu Asp Ser  
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Met Gly Gln Lys Gly His Arg Ile Cys Glu Ile Leu Leu Gln Tyr Leu  
420 425 430

Gln Asp Glu Ser Lys Thr Lys Arg Asn Ser Asp Leu Asn Leu Leu Glu  
435 440 445

Trp Thr His His Ser Met Lys Pro His Glu Ile Pro Gln Gln Leu Asn  
450 455 460

Gly Ser Asp Cys Gly Met Phe Thr Cys Lys Tyr Ala Asp Tyr Ile Ser  
465 470 475 480

Arg Asp Lys Pro Ile Thr Phe Thr Gln His Gln Met Pro Leu Phe Arg  
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<211> 2206  
<212> DNA  
<213> Human

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